

OM of: US-09-805-550-4 to: EST:* out-format : pfs

Date: Aug 31, 2002 4:58 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

```
-MODEL=frame+g2n.model -DEV=x1h  
-O=/cgn2.1/USPTO_spool/US09805550/runat_29082002.160721.29030/app-query.fasta.1.897  
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -GAPOP=4.500  
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blonsum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOR=ext -HEA=SIZE=500  
-MINLEN=0 -MAXLEN=200000000 -USER=US09805550_6CGN1.1.3201  
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TTIMEOUT=120 -WARN_TTIMEOUT=30  
-NO_XLUPX -WAIT -THREADS=1
```

Search information block:

```
Query: US-09-805-550-4  
Query length: 368  
Database: EST*  
Database sequences: 13736207  
Database length: -1841457050  
Search time (sec): 2392.770000
```

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_est1:AV910230	+	894.50	1169.45	632	AV910230 AV910230 K. Sato unpub
gb_est2:BE442895	+	788.50	1031.07	616	BE442895 WHHE1107 A10 B1925 Whea
gb_est2:BG366895	+	729.50	955.90	503	BG366895 HVSMEH002010f Hordeum
gb_est2:BG360535	+	716.50	937.08	605	BG360535 DG1_64_F06_D1 A002 Dad
gb_est2:BE510592	+	704.00	924.64	407	BE510592 946054A04.y1 946 - ta
gb_est1:AV912395	+	652.00	850.33	416	B1927022 EST5456911 tomato flowe
gb_est2:BE510591	-	637.00	832.96	363	BE510591 946054A04.x1 946 - ta
gb_est2:BE510591	-	628.00	819.07	363	B1925179 EST545068 tomato flowe
gb_est1:BE035647	+	612.50	814.75	667	BE035647 MO13A05 MO Mesembryant
gb_est1:AW508593	+	612.50	799.78	689	AW508593 s134a09.y1 Gm-r1030 G1
gb_est2:BG445098	+	612.00	796.50	899	BG445098 GA_Pa0026M08f Gossyp
gb_est2:BG685286	+	604.50	787.64	817	BG685286 EST487049 MHAM Medica
gb_est2:BE1973998	+	602.50	788.20	592	B1973998 sa195d11.y1 Gm-cl065 G
gb_est2:BM113219	+	593.50	774.90	691	BM113219 EST560755 potato roots
gb_est2:BE591983	+	590.50	770.79	704	BE591983 EST499825 P. Infestans
gb_est2:BG447033	+	587.00	763.74	905	BG447033 GA_Eb0040E14f Gossyp
gb_est2:BG650691	+	583.50	764.51	526	BG650691 sad98c06.y1 Gm-cl055 G
gb_est2:BG453539	-	578.50	755.69	663	BG453539 NF093C03LFI1019 Devel
gb_est2:BE704885	-	568.50	740.55	817	BE704885 SC01_02c08.A SC01 AARD
gb_est2:BG045896	+	566.00	739.25	669	BG045896 saad7g06.y1 Gm-cl058 G
gb_est2:BG588991	-	565.00	736.17	801	BG588991 EST490800 MHRP-Medica
gb_est2:BE067283	+	564.50	737.95	626	BE067283 st37g08.y1 Gm-cl067 G1
gb_hic:BC003846	+	564.50	732.06	1137	BC003846 Mus musculus, Stimlat
gb_est2:BE585808	+	561.00	725.61	725	BE585808 Est42p27.E07.e7.051.RS
gb_est2:BE445328	+	557.00	725.60	810	BE445328 GA_Pa0027122f Gossyp
gb_est2:BM271253	+	555.50	727.19	565	BM271253 sak07a10.y1 Gm-cl075 G
gb_est1:AT856811	+	553.00	724.79	517	AT856811 sb78e08.y1 Gm-cl010 G1
gb_est1:AV932070	+	550.50	719.31	647	AV932070 AV932070 K. Sato unpub
gb_est2:BG351432	+	547.00	712.59	804	BG351432 108805 Mature tuber 1a
gb_est2:BG45485	+	541.00	703.85	788	BG45485 GA_Ea0028M06f Gossyp
gb_est2:BE1935539	+	540.50	704.94	830	BE1935539 EST555428 tomato flowe
gb_est2:BG581659	+	540.00	703.81	774	BG581659 EST483334 GVN Medica
gb_est2:BM085128	+	539.50	706.04	578	BM085128 sa12e10.y1 Gm-cl066 G
gb_est2:BG339595	+	538.50	702.97	530	BG339595 EST344022 potato stoid
gb_est2:BE009008	+	536.50	701.39	622	BE009008 ss72b10.y1 Gm-cl062 G1
gb_est2:BG647902	+	534.50	696.47	780	BG647902 EST505921 HOGA Medica
gb_est1:AT726909	+	533.50	698.19	578	AT726909 BN168121 Stx-day G0b
gb_est2:BG586047	+	532.50	694.13	764	BG586047 EST487812 MHAM Medica
gb_est1:AM442310	+	530.50	692.87	666	AM442310 EST311706 tomato fruit

gb_est2:BT750564	-	527.50	688.12	4.4e-29	724	BT750564 Ta01_07c08.R Ta01_A
gb_est2:BE602523	+	527.00	687.32	4.9e-29	735	BE602523 HVSMEH009914f Hord
gb_est2:BG645488	+	525.50	684.42	7.1e-29	808	BG645488 EST507107 KV3 Medic
gb_est2:BG582388	+	524.00	681.92	9.8e-29	854	BG582388 EST484131 GVN Medic
gb_est1:AT901927	-	523.00	686.31	5.6e-29	479	AT901927 618012E05.x1 618 -

seq_name: gb_est1:AV910230

seq_documentation_block:

LOCUS AV910230 632 bp mRNA linear EST 18-JAN-2002
DEFINITION AV910230 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
Baak3m04 5', mRNA sequence.
ACCESSION AV910230
VERSION AV910230.1 GI:18205972
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae
/ Triticeae; Hordeum.
1 (bases 1 to 632)

REFERENCE Sato, K., Saitoh, D. and Takeda, K.

AUTHORS Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadashi Shin-1

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National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

location/Qualifiers

1..632

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Akashinriki"

/db_xref="taxon:112509"

/clone_lib="K. Sato unpublished cDNA library, cv.

Akashinriki vegetative stage leaves"

/tissue_type="leaves"

/dev_stage="vegetative stage"

BASE COUNT 168 a 147 c 166 g 150 t 1 others

ORIGIN

alignment_scores:

Quality: 894.50 Length: 205

Ratio: 4.635 Gaps: 2

Percent Similarity: 94.146 Percent Identity: 84.878

alignment_block:

US-09-805-550-4 x AV910230 ..

Align seg 1/1 to: AV910230 from: 1 to: 632

161 AsphyAsphyValgIn.ArgAlaLeuArgAlaLarAsnAsnProg 177

13 CATAGAGTAAAGCTCAAGAGGCTCTCGGACGCTATACATTCAG 62

177 LuArgAlaValgInLarLeuTySerGlyIleProValThrAlaGluIle 193

63 AACGCGCATGACATCTGATCTGATCTGATCTGATCTGATCTGATCTG 112

194 AlaValProIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 210

113 GCTGTTCCGCGGTTGTCAGGCGGCAACCACTGCTGCACTCTCT 160

210 rGlyIuAlaGlyLeuSerGlyIleProAsnThrAlaProLeuAspLeu 227

161 GCAGAACTGCGCTCTGATCTGATCTGATCTGATCTGATCTGATCTT 209

227 heProGInGlyAlaSerAsnAlaGlyGlyGlyGlyGlyGlyGlyGly 243

seq_name: gb_est2:BE442895	seq_id: BE442895	seq_size: 616 bp	seq_type: mRNA	seq_desc: linear EST 25-JUL-2000
seq_documentation_block:	LOCUS	BE442895		
DEFINITION	WHE1107_A10_B19S	wheat etiolated seedling root normalized cDNA library	Triticum aestivum	CDNA
ACCESSION	BE442895			
VERSION	BE442895.1	GI:9442418		
KEYWORDS	EST.			
SOURCE	bread wheat.			
ORGANISM	Triticum aestivum			
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticaceae; Triticum.			
ADTHORS	1 (bases 1 to 616)			
TITLE	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Izzo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.			
JOURNAL	The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library			
COMMENT	Unpublished (2000)			
FEATURES	Source			
source	1..616			
	/organism="Triticum aestivum"			
	/cultivar="Chinese Spring"			
	/db_xref="taxon:4565"			
	/clone="WHE1107_A10_B19"			

```

/clone.lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/notes="Vector: lambda uni-zap XR, excised phagemid
phascript SK: Site.1: EcoRI; Site.2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and ceftaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in
TJ Clonase lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give phuscript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HP Nguye
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)".
```

BASE COUNT 161 a 158 c 153 g 143 t 1 others

ORIGIN

Alignment_scores:

Quality:	788.50	Length:	206
Ratio:	4.239	Gaps:	3
Percent Similarity:	90.291	Percent Identity:	75.728

alignment_block:

US-09-805-550-4 x BE442895 ..

Align seg 1/1 to: BE442895 from: 1 to: 616

```

39 TyrProTPrGlyGngInleuLeuIlePhaSnGlyVysValleuYas 55
|||||
3 TATCCATGGGTCACCAACCTGCTGATTCACACAGCGCAAGGTTTGAAGA 52
|||||
55 pGluSerThrLeuGluGlnuAnlysValaGlnuAspGlyPheLeuVal 72
|||||
53 TGAAGACCACTGGATGAAATCAAGTTACGAGAAAGATGATTTCTAGTTG 102
|||||
72 aMetLeuSerLysGlyLysThrSerGlySerThrGlyThrSerSerSer 88
|||||
103 TCATGCTTAGCAAGATGAAGCTTCTCTCCAGTGAGAGCTTCATCTGCG 152
|||||
89 GlnHisSerAsnThrProAlaThrArgGlnAlaProProLeuGlnAla 105
|||||
153 CAGCCCTTCACGACCTCGTTACCAAGTCAAGCACTCCGACGTTCCAAAC 202
|||||
105 oGlnGlnAlaProGlnProProValAlaProIleThrThrSerGlnPro 122
|||||
203 A...CAAGCTCTCAGCCGCCAGGCTCCATCACTACGACTTCTCAGCCTG 249
|||||
122 InGlyLeuProAlaGlnAlaPro...AsnThrHisAspAsnAlaLeuSer 137
|||||
250 AAAAGACCAACCGGAGAGACCCCTTCGAGTGTGATCTTGGAGCATCG 299
|||||
138 AsnLeuLeuSerGlyArgAsnValAspThrIleIleAsnGlnLeuMet 154
|||||
300 GATTYACTAGTCAGAGAACCAATCTGGACACATATATTAAACAGATATGGA 349
|||||
154 uMetGlyGlyGlySerThrPaspAspLysValGlnAlaGlnAlaLeuArg 171
|||||
350 GATGGGGGGGTGGCAGCTGGGACAGAGATTAAGCTCCAAAGAGCTCTCGG 399
|||||
171 laaIaTyAsnAsnProGluArgAlaValGluTyArgLeuTySerGlyIle 187
|||||
400 CTGCTTAAACAATCCAGAAACGGCCATTACATCTGTAACCTGTGTATT 449
|||||
188 ProValThrAlaGluIleAlaValProIleGlyGlyGlnGlyAlaAsnTh 204
|||||

```

```

450 CCAGTGCACGCTGGAGTTGTCTGTCCCGTGCTTGGTCGAAGGGGCCAAACAC 499
204 rThrsAspaGaLaAProTHrGLyLuAaGLyLeusErgIlylPProASnt 221
||||| |||||::: |||||::: |||||::: |||||::: |||||:::
500 CACTGATGCAGCCTCCGNA...GAAACCGGCCTCTCTGTAATCCCAACA 546
221 hPaLAProLeuAspLeuPhenProGLngLYAlaSerAsnLaGLyGLy 237
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
547 CAGCACCATTAATATTCTTTCCACAGGGGGCTCCATCTGAGAGTGTCT 596
823 ATAGLyGLyProLeu 243
::: ||||| |||
597 GTGGGGGGGTGCATCTT 614

seq_name: gb_est2.BG368695

seq_documentation_block:
LOCUS BG368695 503 bp mRNA linear EST 22-Oct-2001
DEFINITION HVSME10020E10f Hordeum vulgare 20 DAP spike EST library HvCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSME10020E10f, mRNA sequence.
ACCESSION BG368695
VERSION BG368695
KEYWORDS
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 503)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Fritsch,D., Yu
,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol,D.W., Fenton
,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomes: Morex 20 DAP spike cDNA library
Unpublished (2001)
On Mar 8, 2001 this sequence version replaced gi:1325796.

JOURNAL
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 475
Seq primer: AATTACCCTCCTCAAGAAGG
High quality sequence stop: 503.

FEATURES
Source
1..503
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME10020E10f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HvCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; site_1: EcoRI; site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 20 DAP (Fenton
). Total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give plasmid SK(-) cDNA
phagemids in the TJ Close lab at the University of
California, Riverside (Chol). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
```

REFERENCE 1 Clade: Panicoidae; Andropogoneae; Sorghum.
 (bases 1 to 605)
 Cordonier-Pratt, M., Gingle, A., Marsala, C., Sudman, M. and Pratt, L.H.
 An EST database from Sorghum: dark-grown seedlings
 TITLE Unpublished (2000)
 JOURNAL Department of Botany
 COMMENT Contact: Cordonier-Pratt MM
 The University of Georgia
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 542 1805
 Email: mmpatr@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
 Seq primer: JEN REV
 High quality sequence stop: 567
 POLYA-No.

FEATURES
 source Location/Qualifiers
 1. 605
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Dark Grown 1 (DG1)"
 /note="Organ: 5-day-old dark-grown seedlings. Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector Lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 166 a 178 c 152 g 109 t
 ORIGIN

alignment_scores:
 Quality: 716.50 Length: 152
 Ratio: 4.841 Gaps: 1
 Percent Similarity: 97.368 Percent Identity: 92.763

alignment_block:
 US-09-805-550-4 x BE360535 ..

Align seg 1/1 to: BE360535 from: 1 to: 605

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1 Mettyleuethrvallysthrleuylsglythrhishegluilearqva 17
|||||
148 ATAAAGCTGACGGTGAAGACCCCTCAAGGGCACGACCTCGAGATCCGGGT 197
|||||
17 Tglnproasaspthrilemetalaavallyslyasnllegluilleg 34
|||||
198 CGAGCCCAAGACACGATTTGGCTGTGAAGAGAACATGCAAGAGATAC 247
|||||
34 Tngilyasaspserlyrprotrpglynglnleuleuilepheasnngly 50
|||||
248 AAGCAAGAGGACACTATCCATGGGGGCAACACTGCTGATTTCAATGGG 297
|||||
51 Lysvalleuylaspgluserthrleugluasnllysalasngluas 67
|||||
298 AAGGCTCTGAAGATGAAGTACATTGAGAGATAAATAAAGCAAGA 347
|||||
67 pgilyphelauvalmetleuerysglylysthrserglyserthrg 84
|||||
348 TGGGTTTCTGTGTCTCATGCTTAGTAAGGTTAAACATCTGGTTCAAGTG 397
|||||
84 LyrthrserSerSerGlnHisSerAsnThrProAlaThrArgGlnAlaPro 100
|||||
398 GAACCTTCATCTCCAGCCCTCAACACCTCTGACAGCAAGGACGACCT 447
|||||
101 FrcleugluAlaProGlnGlnAlaProGlnProProValAlaProIleth 117
|||||
448 CCGTGTGATGCCCCACAAAGTCCCTCACGCCCGGTGGCACCACACTAC 497
|||||
117 rThrSerGlnProGluGlyLeuProAlaGlnAla...ProAsnThrHis 133
|||||
498 AACTTTCAGCTGAAAGGACTTCTGACACAGGCTCCTCTTAACACATATG 547

```

133 spasnalaaserasnleuenserglyarqsnvalasprhilleile 149
 |||||
 548 ACAATGCAGCATCAATGCTTCTATCAGGAAGCAATGTTGACACATATAT 597
 |||||
 150 Asngln 151
 |||||
 598 AACCG 603

seq_name: gb_est2:BE510592

seq_documentation_block:
 LOCUS BE510592 407 bp mRNA linear EST 07-AUG-2000
 DEFINITION 946054A04.y1 946 - tassal primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION BE510592
 VERSION BE510592.1 GI:9731840
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade: Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 407)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946054 row: A column: 04.

FEATURES
 source Location/Qualifiers
 1. 407
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="946 - tassal primordium prepared by Schmidt
 lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XLOLR"
 /note="Organ: tassels. Vector: HybriZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between Imm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 kb with a 1 kb average."

BASE COUNT 134 a 91 c 95 g 87 t
 ORIGIN

alignment_scores:
 Quality: 704.00 Length: 135
 Ratio: 5.215 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-805-550-4 x BE510592 ..

Align seg 1/1 to: BE510592 from: 1 to: 407

```

28 Lysasnilleugluilegnglylsaspserlyrprotrpglynglnl 44
|||||
2 AAGAATATTTGAAGATGAAGGAAAGCAACACTATCCATCAGGGCCACA 51
|||||
44 nleuilellepheasnnglylsvalleuylaspgluserthrleuglng 61
|||||
52 ACTGCTGATTTCAATGGAAGGCTTGAAGATGAAGATGATGATGAG 101

```

```

61 luasnlyrsValaIngluAspGlyPheLeuValaMetLeuSerLyseGly 77
   |||||
102 AGATAAAGCAATGAGATGGGTTTCTAGTTGCTAGTCTAGTAAGAGGT 151
   |||||
78 LysThrSerGlySerThrGlyThrSerSerSerGlnHisSerAsnThrPrp 94
   |||||
152 AAAACAATCTGTTCACTGCACTGCACTTCCTCCAGCAGCTCAAACTCC 201
   |||||
94 oAlaThrArgGlnAlaProLeuGlnAlaProGlnAlaProGlnAlaProGln 111
   |||||
202 TGCACACAGCAGCAGCAGCTCTCTAGAGGCCCAACACAGCTCTCAAC 251
   |||||
111 roProValAlaProIleThrThrSerGlnProGlnGlyLeuProAlaGln 127
   |||||
252 CCCGGTGGCAGCAATTAACAATCTCAGCCTGAAGAGCTCTGACAG 301
   |||||
128 AlaProAsnThrHisAspAsnAlaAlaSerAsnLeuSerGlyAlaArg 144
   |||||
302 GCACCTTAACACACATGCAATGCGCATCAATCTCTCTGAGAGGAA 351
   |||||
144 nValAspThrIleIleAsnGlnLeuMetGluMetGlyGlySerThrPa 161
   |||||
352 TCTTGAACACATATTAATTAACCACTAATGACATGGTGGGAGATTGGG 401
   |||||
161 spLys 162
   |||||
402 ACAA 406

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seq_name: gb_est2:BI927022

seq_documentation_block:

LOCUS BI927022 771 bp mRNA linear EST 18-OCT-2001
 DEFINITION EST546911 tomato flower, 3 - 8 mm buds Lycopersicon esculentum cDNA
 clone cTOB21A11 5' end, mRNA sequence.
 ACCESSION BI927022
 VERSION BI927022.1 GI:16236126
 KEYWORDS EST.

SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.

REFERENCE 1 (bases 1 to 771)
 van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
 Uiterback,T., Van Aken,S., Ronning,C.M., Niemman,W., Fraser,C.M.,
 Martin,G.B., Giovannoni,J.D. and Tanksley,S.D.
 Generation of ESTs from tomato flower tissue, 3-8 mm buds (2001)

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Unpublished (2001)
 Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: 73.

FEATURES
 source
 Location/Qualifiers
 1..771
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cTOB21A11"
 /clone_lib="tomato flower, 3 - 8 mm buds"
 /tissue_type="flower"
 /dev_stage="3-8mm buds"
 /note="Vector: pBluescript SK(-); site_1: EcoRI; site_2:
 XhoI; supplier: Cornell University; sequencing: The
 Institute for Genomic Research. Flower buds and flowers
 were taken from greenhouse plants (4-8 wks old, TA496).
 They were immediately frozen in liquid nitrogen and then
 size-separated while remaining frozen."

seq_name: gb_est1:AV912395
 seq_documentation_block:

BASE COUNT 213 a 160 c 180 g 218 t
 ORIGIN

alignment_scores:
 Quality: 652.00 Length: 228
 Ratio: 3.505 Gaps: 6
 Percent Similarity: 81.579 Percent Identity: 61.842

alignment_block:
 us-09-805-550-4 x BI927022 ..

Align seg 1/1 to: BI927022 from: 1 to: 771

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1 MetLysLeuThrValaLysThrLeuLysGlyThrHisPheGluIleArgVa 17
   |||||
101 ATGAAGCTCACTGTAAAGACTCTCAAGGGAAGTCACTTGAATAATAGGT 150
   |||||
17 LglnProAsnAspThrIleMetAlaValaLysLysAsnIleGluIleG 34
   |||||
151 TCAGCATCTGTATAGATTAATGAGCAGTCAAGAAAGACATTGAAGATGAC 200
   |||||
34 LngLysAspSerThrProThrPglGlnGlnLeuIlePheAsnGly 50
   |||||
201 AAGGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 250
   |||||
51 LysValLeuLysAspGlySerThrLeuGlnLysValaIngluAs 67
   |||||
251 AAAGTGTGCTGAAGATGAAGATCAATTTGTTGAAAAACAATGCTCTGAGGA 300
   |||||
67 pGlyPheLeuValaValaMetLeuSerLysGlyLysThrSerGlySerThr 84
   |||||
301 TGGTTTCTGTTGTCATGCTTACAGCAAGCAAAACTCTAGCTCAAGTG 350
   |||||
84 LysThrSerSerGlnHisSerAsnThrProAlaThr..ArgGlnAla 99
   |||||
351 GGACAACTTCTGCTCAGCAGCAGCACTGCCCAATCTCACTAACAACA 400
   |||||
100 ProProLeuGlnAlaProGlnAlaProGlnProProValAlaProIle 116
   |||||
401 CTGTAAGTATTCGCGCATCAACAGGCCCAAA..GATGTTGTCTGACG 447
   |||||
116 eThrThrSerGlnProGlnGlyLeuProAlaGlnAlaProAsnThrHis 133
   |||||
448 TTGGATGCTCGCGCTGCTAGCTTCCAGCT.....GATGATTATA 488
   |||||
133 spAsnAlaAlaSerAsnLeuSerGlyArgAsnValaAspThrIleLe 149
   |||||
489 GTCAAGCTGCATCAAAATTAATTAATTAATTAATTAATTAATTAATTA 538
   |||||
150 AsnGlnLeuMetGluMetGlyGlySerThrPaspLysAspLysValG 166
   |||||
539 CAACAACCTTAATGAATGATGGTGGTGGCAGCTGGCAAGAGACAGTTAC 588
   |||||
166 nArgAlaLeuArgAlaAlaLysAsnProGlnArgAlaValaGluIle 183
   |||||
589 TCGTCACTTCGAGCTGCTTAACCAATCTGAAGAGCTGTGATACT 638
   |||||
183 eutySerGlyIleProValThrAlaGluIleAlaValProIle.GlyG 199
   |||||
639 TATATTCAGGAATTCCTGAACGGAAGTTCTGTGTCGGTAGGCGG 688
   |||||
199 yGlnGlyAlaAsnThrThrAspArgAlaProThrGlyGlu.....AlaG 214
   |||||
689 GGGTGCATTAATCTGCT...GCTGTGCTACACCTGCGCTATGACAC 735
   |||||
214 LysLeuSerGlyIleProAsnThrAlaProLeu 224
   |||||
736 CTCTCTTGGGCACTTAATCTGCTTGA 767

```

LOCUS	AV912395	614 bp	mRNA	linear	EST 18-JAN-2002
DEFINITION	AV912395 K. Sato unpublished cDNA library, cv. Akashinriki				
ACCESSION	BA630043.1, mRNA sequence.				
VERSION	AV912395.1 GI:18208172				
KEYWORDS	EST.				
SOURCE	Hordeum vulgare subsp. vulgare.				
ORGANISM	Hordeum vulgare subsp. vulgare.				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.				
AUTHORS	Sato, K., Saitoh, D. and Takeda, K.				
TITLE	Bailey EST sequencing project in NIG and Okayama Univ				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Tadasu Shin-1 Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tsuhin@genes.nig.ac.jp.				
FEATURES	location/Qualifiers				
source	1..614				
	/organism="Hordeum vulgare subsp. vulgare"				
	/cultivar="Akashinriki"				
	/db_xref="taxon:112509"				
	/clone="baak3m04"				
	/clone_lib="K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves"				
	/tissue_type="leaves"				
	/dev_stage="vegetative stage"				
BASE COUNT	163 a 152 c 119 g 177 t 3 others				
ORIGIN					
alignment_scores:					
Quality:	637.00	Length:	143		
Ratio:	4.684	Gaps:	0		
Percent similarity:	95.105	Percent identity:	84.615		
alignment_block:	US-09-805-550-4 x AV912395/rev ..				
Align seg 1/1 to reverse of:	AV912395 from: 1 to: 614.				
226	leuphepGgInglYAlaseRnaAlaGlYGLYAlaGlYGLYpR 242				
613	CTTTTCCCGCAGGGGCTCCATGCTGGAGGCTGCTGCTGGATC 564				
242	oieuasphleuAtrgAsnAsnProGlnpheGlnAlaValatrgLumety 259				
563	ACTTGATTTTCTTCGAATATACCAACAGATTTCACGACATTCGGGAATG 514				
259	alnHstrhrsnProGlnlleuGlnPrometleuValGluLeuSerlyS 275				
513	TCCATPCCAATCCACAAATTTTACACNATATGCTCCAGGAATTTGACCAAG 464				
276	GlnAspProGlnlleuAtrgLeuileGluGluAsnHisAspGluPhe 292				
463	CAGAACTCTCAACTTCTTAAGTTGATTCAGAGAACAAATGATGATTCCT 414				
413	TCAGTACGAAATGACACATTTGAAGCGGCGCATGGGCACTTTGAGAC 364				
309	lnProGluGluAspGluMetProHisAlaIleSerValThrProGluGlu 325				
363	AGGCTGACCAAGATGGAAATGCCCTCAATCATCATGATGACACCAAGAG 314				
326	GlnGluAlaIleGlyAtrgLeuGluSerMetGlyPheAspArgAlaArg 342				

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313 CAAGAGGCATTGGAAAGCTTGAAGCCATGCGGCTTTGAGAGACACAGGTGT 264
342 111egua1aphelueuAlacysaparrgsangluluenuAlalaasnt 359
|||||.....
263 CACGGAAGCATTCCTTGCGCTGTGACAGAGATGAGCAACTGCTCAAAC 214
359 yrlenuengluHlsA1aglygluJasp 368
|||||.....
213 ATCTTTTGAGCATGCTGTGTGACGAAGA 185

seq_name: gb_est2:BE510591

seq documentation block:
LOCUS BE510591 365 bp mRNA linear EST 07-AUG-2000
DEFINITION 946054A04.x1 946 - tassal primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BE510591
VERSION BE510591.1 GI:9731839
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 365)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
FEATURES
Table: 946054 row: A column: 04.
source Location/Qualifiers
1..365
/orrganism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EORI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 94 a 99 c 77 g 95 t
ORIGIN
alignment_scores:
Quality: 633.00 Length: 121
Ratio: 5.231 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805--550-4 x BE510591/rev ..

Align seg 1/1 to reverse of: BE510591 from: 1 to: 365

223 ProleuaspleneuhPrognlglayalasearnalaglYcylayalagl 239
|||||.....
363 CCACGTGATCTTTTCCCGCAGGGGCTTCGAATGCTGAGGTGCTCTGG 314
239 yglYgYlProleuasPpheleuargrnsnPrroGlnphneGlinalaya1a 256
|||||.....
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source
1. 689
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-785"
/clone_lib="Gm-r1030"
/lab_host="DH10B"
/notes="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
cDNA library was constructed from mRNA isolated from
immature cotyledons of greenhouse grown plants
(individual seed fresh weight of 100-300mg). The library
was prepared using the Life Technologies pSuperscript cDNA
library construction kit. Complementary DNA was
synthesized from mRNA using a poly(dT) sequence with a
NotI restriction site. SalI linkers adapters were ligated
to the blunt-ended cDNA fragments followed by NotI
digestion. The cDNA fragments were directionally cloned
into the NotI-SalI restriction site of the pSPORT1
vector. The ligated cDNA fragments were transformed into
E. coli Electromax DH10B host cells. This library was
constructed by Dr. Lila Vokkin and Dr. Anu Khanna. Note
that Gm-r1030 is a re-track of Gm-cl007."

BASE COUNT      175 a      168 c      169 g      177 t
ORIGIN

alignment_scores:
Quality: 612.50      Length: 228
Ratio: 3.422      Gaps: 4
Percent Similarity: 78.509      Percent Identity: 58.772

alignment_block:
US-09-805-550-4 x AWS08593 ..

Align seg 1/1 to: AWS08593 from: 1 to: 689

136 AlaserasnleuSerGlyArgAsnValAspThrIleIleAsnGlnLeu 152
|||||
1 GCATCTATATCTGTGCTGGAAGTAACTGTGAGGGAACCATTCGCAAT 50
|||||
152 uMetGluMetGlyGlySerTrpAspIleValAspGlnArgAlaL 169
|||||
51 CCTTGACATGGTGAGAGAGCTGCGACAGGATCTGCTTCGCTC 100
|||||
169 euArGAlaAlaIArgAsnAsnProGluArgAlaValGluTyrLeuTyrSer 185
|||||
101 TTGCTGCTGCTATACACCTGAGAGAGCTGTGATATTGTTATTC 150
|||||
186 GlyIleProValThrAlaGlu.....IleAlaValProIleG1 198
|||||
151 GGCATTAACCAAGACAGCTCAAGCTCCACGCTTACCAGAGCTGCAAG 200
|||||
198 yGlyGlnGlyAlaAsnThrThrAspArgAlaProThrGlyGluAlaGlyL 215
|||||
201 TGCTCAACCTGCAAAATCCCTCAGCTGCTGCCACAGCAGCAACACAG 250
|||||
215 eu.....SerGlyIleProAsnThrAlaProLeuAsnProLeuPro 228
|||||
229 GlnGlyAlaSerAsnAlaGly...GlyGlyAlaGlyGlyGlyProLeuAs 244
|||||
301 CAGGGCTTCCAAATGTTGGTCTGCTGCTGCTGCTGCTGCTTTAGA 350
|||||
244 PheLeuArgAsnAsnProGlnPheGlnAlaValArgGluMetValHisT 261
|||||
351 CTTCCTTCGACACAGTCACAGCTTACGCGCATATGTTACAGG 400
|||||
261 hArgAsnProGlnIleLeuGlnProMetLeuValGluLeuSerTyrGlnAsn 277
|||||
401 CTATATCCAAATAATTCACCTATGCTACAGAGCTTGCAACAAAT 450
|||||
278 ProGlnIleLeuArgLeuIleGluGluAsnHisAspGluPheLeuGlnLe 294
|||||

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451 CCTCATCTTATGCATTCGATTCAAGACATCACTGTGACTTCCTCCCT 500
294 uLeuAsnGluProPheGluGlyGlyGlyGlyAspPheLeuAspGlnPro 311
|||||
501 AATTAATGAACCCCTGTGAGGGGTGAGGGAATATATCTGGAGACAG...C 547
|||||
311 lGluAspGluMetProHisAlaIleSerValThrProGluGluGlnGlu 327
|||||
548 TAGCTAGTGCATTCGCCACACAGTACAGTACACCCCTGAGGAAGG.CAA 596
|||||
328 AlalleGlyArgLeuGluSerMetGlyPheAspArgAlaArgValIleG1 344
|||||
597 GCAATTTGACGCTCTCGAAGCAATGGGATGATGCTGCACTGATTTGA 646
|||||
344 uAlaPheLeuAlaCysAspArgAsnGluGluLeu 355
|||||
647 GGTGTACTCTGCTGTGTCATCAAAATGAGGAGACTG 680
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seq_name: gb_est2:BG445098

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seq_documentation_block:
LOCUS      BG445098      899 bp      mRNA      linear      EST 15-MAR-2001
DEFINITION GA_Ea0026M08f Gossypium arboreum 7-10 dpa fiber library Gossypium
ARBOREUM cDNA clone GA_Ea0026M08f, mRNA sequence.
ACCESSION  BG445098
VERSION    BG445098.1 GI:13354750
KEYWORDS   EST.
SOURCE     Gossypium arboreum.
ORGANISM   Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE  1 (bases 1 to 899)
AUTHORS   Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
JOURNAL   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: TATACGACTCACTATAGG
High quality sequence stop: 772.
Location/Qualifiers
1..899
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0026M08f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/notes="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

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BASE COUNT      256 a      206 c      215 g      221 t
ORIGIN

alignment_scores:
Quality: 612.00      Length: 301
Ratio: 2.873      Gaps: 9
Percent Similarity: 70.764      Percent Identity: 46.844

alignment_block:
US-09-805-550-4 x BG445098 ..

Align seg 1/1 to: BG445098 from: 1 to: 899

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26 VALLVSLYSASNIIIEGLUUIIEGLINGLYLSASPSETYRPROTPGL 42
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10 GTAAAAAGACATAGAAACTGTTCAGGACTGATTATCCCTGCTTC 59
   |||||
42 YGINGLNULEULEPHEASNGLYLSVALLEULYSASPGIUSERTHL 59
   |||||
60 ACAACAAATGCTATCTATTAAGGAAAGTCTTTAAAGTGCACAGCAC 109
   |||||
59 EUGLUASNLUSVALSANGIUSAPGYPHELEUVALMETLEUSER 75
   |||||
110 TGGCTGAAAACAGTGTCACTGAAATAGCTTATGTCATCATGTTAACA 159
   |||||
76 LYSGLYLYSTHRSERGLYTHRSERGLYTHRSERGLYTHRSERGL 92
   |||||
160 AAGAAATTAAG.....GGTACAACTGGTGAGGGTTCAACT.....GCTTC 197
   |||||
92 NTHRPROLATHRARGINALAProProleuGLUALAProGINGLNALA 109
   |||||
198 AACAGCTCCTNCAAGAAAGCTCTGAGGCAAGTATCGCCACAGCTC 247
   |||||
109 TROGLNPRO...ProVALAProLIEPHTHRSERGLN..... 120
   |||||
248 CAGCACACAGCTTCTACTGCACCTGTTCGCAACGCTGATGCTGCAGCT 297
   |||||
121 .....ProGLUGLYLEUProGLAAGLINALAProAS 130
   |||||
298 GCCACTGAATGCTCTGCTGCTTCAAGTACTCTTCTGCTCAGATTCGA 347
   |||||
130 NTHRHSASPNALALASERASNLEUSERGLYARGASNAVALASPT 147
   |||||
348 TGTATATGGCCAGCAGCATCTAACCCTGGTTCAGGAGTACTAGAGG 397
   |||||
147 HTLEILEASNGIUEUWETGLUWETGLYGLYGLYGLYGLYGLYGLY 163
   |||||
398 GAACAATCAACAGATCTGTGATGATGGGAGGAGCACTGGGACAGGAC 447
   |||||
164 LYSVALGINARGALALEUARGALALATYRASNANPROGLIARALAY 180
   |||||
448 ACTGTGTGCCACGCCCTTGCTGCTCTTATATTAATTAACCCAGAGAGCTGT 497
   |||||
180 IGLUITYRLEUTYRSEGLYILEPROVALTHRALAGLU.....I 193
   |||||
498 TGAATATTTGATTTCTGGCATCCCGAGCAAGCTGACAGCTGCCTGG 547
   |||||
193 LEALVALPROILEGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 207
   |||||
548 CCCGTGCTCTGTAGTGGGCAACCAACCTGCTGCACCAACCTCA 597
   |||||
208 .....ALAPROTHRGLYLUAGLYLEUSERGLYILEPROASNTHRAL 222
   |||||
598 CAGCCTGCACAAACGGCAGCTATTCCTGCACAGTGA...CCAAATGCAAA 644
   |||||
222 APROLEUASPLEUPHEPROGLINGLYLASERASNALAGLY...GLYGLYA 238
   |||||
645 TGCATTAGACCTCTTCCCAAGGGCTTCCCAACATGGGTGCAATGGTG 694
   |||||
238 IAGLYGLYGLYPROLEUASPHLEUATARGASNANPROGLINPHEGINALA 254
   |||||
695 CTGAGGCTGGGACCTCTTGATTTTACGAAACAGTACACAGTTTCAAGCT 744
   |||||
255 VALARGIUMETVALHISTHRASNPROGLINLEUGINPROMETLEUVA 271
   |||||
745 TTGCGAGCAATGTCGCAAGCCATCCAAATATTGGAGGCCATCTTCA 794
   |||||
271 IGLULEUSERLYSGINASNPROGLINLEU...ARGLEUIEGLUUSN 287
   |||||
795 AGGAGTGGGGAANCAAAATGCTAATTATGAAAATATACAGAGAGCT 844
   |||||
288 HISASPGIUPHELEUINLEUASNGIUPROPHGLUGLYGLYGLU 304
   |||||
845 CAGGCTGATTTCTTCTGATCAAGAACCTGCGTGGGAGGAGG 894
   |||||
304 Y 304

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```

seq_name: gb_est2:BG585286
895 A 895
seq_documentation_block:
LOCUS      BG585286                817 bp    mRNA    linear    EST 11-APR-2001
DEFINITION EST487049 MHAM Medicago truncatula/Glommus versiforme mixed EST
ACCESSION  BG585286
VERSION    BG585286
KEYWORDS   Medicago truncatula/Glommus versiforme mixed EST
SOURCE     Medicago truncatula/Glommus versiforme mixed EST library.
ORGANISM   Eukaryota; mixed EST libraries.
REFERENCE  1 (bases 1 to 817)
AUTHORS    Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
           and Fraser,C.M.
TITLE      ESTs from roots of Medicago truncatula after colonization with
           Glommus versiforme, 2001
JOURNAL    Unpublished (2001)
COMMENT    Contact: Harrison M.J.
           Plant Biology Division
           The Samuel Roberts Noble Foundation
           2510 Sam Noble Parkway, Ardmore, OK 73401
           Tel: 580-223-5810
           Fax: 580-221-7380
           Email: mjharrison@noble.org
           Noble EST name: N380759e TIGR sequence name: MFDGB837K More
           information is available at: http://www.medicago.org
           Seq primer: Skmod (CTA gaa cta gac gat cc).
FEATURES
   source
       1..817
       /organism="Medicago truncatula/Glommus versiforme mixed EST
       library"
       /cultivar="Medicago truncatula genotype A17"
       /db_xref="taxon:119092"
       /clone="pNHAM-22M22"
       /clone_id="NHAM"
       /tissue_type="roots colonized with Glommus versiforme"
       /dev_stage="roots harvested at 10, 17, 22, 31 and 38 days
       post-inoculation with Glommus versiforme. The library was
       made from a mixture of RNA from each of these stages."
       /lab_host="E. coli strain XL0LR"
       /note="Vector: pBluescript SK-. Site.1: EcoRI; Site.2:
       XhoI; cDNA was prepared from polyA+ enriched RNA from
       roots harvested at 10, 17, 22, 31 and 38 days
       post-inoculation with Glommus versiforme. The cDNA was
       directionally ligated into the UniZap XR vector from
       stragene and packaged using GigaPack III Gold packaging
       extracts. Plasmids containing cDNA inserts were excised
       from the recombinant lambda-Zap phage using Ex-assist
       helper phage and propagated in XL0LR cells."
BASE COUNT      229 a      217 c      178 g      193 t
ORIGIN
alignment_scores:
  Quality: 604.50      Length: 283
  Ratio: 2.906
  Percent Similarity: 73.498      Percent Identity: 49.470
alignment_block:
US-09-805-550-4 x BG585286
Align seg 1/1 to: BG585286 from: 1 to: 817
64 VALASNGIUSAPGYPHELEUVALMETLEUSERLYSGLYLS..... 78
   |||
7 GTTCTGAGAAATAGTTTATGTCATCATGTTGCCAAGAAATAGCTATC 56
   |||
79 .THRSERGLYSTHRSERGLYTHRSERGLYTHRSERGLYTHRSERGL 95
   |||

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57 ATCAAGTGGAGCCCTGCTGCTCAGCTGCCGCCACGGCAGTCCACCTG 106
95 laThrArgGlnAlaProProLeuGlnAlaProGlnGlnAlaProGlnPro 111
107 CAAGTCTTTGGCTCTTGTTCACACCTCTAG..... 141
112 ProValAlaProLeuThrThrSerGlnProGlnGlnLeuProAlaGln.. 127
142 CCGTCTCTTCA...ACTGTGGACAGGAGAAATCCAAATCTGGCGCAGG 188
128 .....AlaProAnThrHisAspAsnAlaAlaSerAnLeuLeus 141
189 TCGCTGTGTACTCTCCCACTACTGTGGGCCGATCTATCTCATGTG 238
141 erGlyArgAnValAspThrIleIleAsnGlnLeuMetGlyGly 157
239 CTGGAACTTGTAGAACCACTATTCACAAATTCAGAAATGGGGGA 288
158 GlySerTrpAspLysAspLysValGlnArgAlaLeuArgAlaAlaIyrAs 174
289 GGAAGTGGGATCGGACACTGTGATCCGAGCTCTGTGCTGCATATAA 338
174 naaProGlnAlaArgAlaValGlnIyrLeuIyrSerGlyIleProValThra 191
339 CAATCCCGAAAGAGCGGTGATATCTATCTGGCATGCCGACACAG 388
191 laGlu.....IleAlaValProIleGly...GlyGlnGlyAlaAsn 203
389 CTGAAGCTCCAGACGTTGTCATCCACCAATGTGGGACGGCAAAAC 438
204 ThrThrAspArgAlaProThrGlyLysAlaGlyLeuSerGlyIleProAs 220
439 CCTTCACCCAGGCTCCAGCCCACTAGCTGTGCTGTGGGCCCAA 488
220 nThrAlaProLeuAspLeuPheProGlnGlyAlaSerAsnIaGlyGlyG 237
489 CACCAACCCACTTAACTTGTCCCTCAGGCGCATCCCAATTTGGGTGCA 538
237 LysAlaGlyGlyGlyProLeuAspPheLeuArgAsnAsnProGlnPheGln 253
539 ATGAAATGCGAGTGTGAAATCTCGCAAAACAGTCACAGTCCAA 588
254 AlaValArgGlyMetValHisThrAsnProGlnIleLeuGlnProMetLe 270
589 GCCTTGGAACAATGTGCAAGCAACCTCAATCTTACAGCCATGCT 638
270 uValGlnLeuSerLysGlnAsnProGlnIleLeuArgLeuGlnGlnG 287
639 TCAGAACTAGGAAACAAATCCAAACCTATATGGAATCTATCCAGAGC 688
287 snHisAspGluPheLeuGlnLeuLeuAsnGlnProPheGlnGlyGlyG 303
689 ATCAAGCTGACTTCTTACGCTCTTATAATAGCCT.....GGAGGCGAA 732
304 GlyAspPheLeuAspGlnProGlnGlnAspGlnMet.....Pr 316
733 GAGAACTTA.....GAGGAGACAGTATAGTGTGCTTGGCTCC 767
316 ohHisAlaIleSerValThrProGlnGlnGlnAlaIleGlyArgLeu 332
768 TCAGACCACTACTATACACCCAGAAAGAGAGAGAGCCATTCACAGGCTT 816

seq_name: gb_est2:BI973998

seq documentation block:
LOCUS BI973998 592 bp mRNA linear EST 30-NOV-2001
DEFINITION sal15d11.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-8637 5' similar to TR:003991 003991 RAD23 PROTEIN,
ISOFORM II, mRNA sequence.
ACCESSION BI973998
VERSION BI973998.1 GI:16348403
KEYWORDS EST.
SOURCE soybean.

```

```

ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 592)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,R., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Rohm,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800) 533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
1..592
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-8637"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/note="Vector: Bluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT 176 a 125 c 128 g 163 t
ORIGIN
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Quality: 602.50 Length: 197
Ratio: 3.742 Gaps: 2
Percent Similarity: 81.726 Percent Identity: 60.914
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US-09-805-550-4 x BI973998 ..
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22 TlleMetAlaValLysLysAsnIleGlnGlnIleGlnLysAspSerT 39
|||||
52 TGTATGTGCTGTCAAGAAATATTGAAGATGTACAAAGAAAGATTAATT 101
39 YrProTrpGlyGlnGlnLeuLeuIlePheAsnGlyLysValLeuLysAsp 55
|||||
102 ACCCATGTGCACAGCAATTTGTTGATTCACATGCGAAGCTTTTGAAGAT 151

```

56 GluSerThrLeuGluGlnAsnLysValAsnGluAspGlyPheLeuVal₇₂
|||||
152 GAACACTGACCTTAGAGATTAAGCTCTGAAAGAGCGCTTCTGTTG₂₀₁
72 MetLeuSerLysGlyValSerGlySerGlyThrSerGlyThrSerSerG₈₉
|||||
202 TATGCTTAAAGATTAAGATCAATCAGTTGCTGCAAGCTCTGCTTC₂₅₁
89 LHisSerAsnThrProAlaThr.....ArgGlnAlaPro₁₀₀
|||
252 AGCTGCGCAGTAACTCTCTACGACTGATCAACGTCAAAATTCACCGCT₃₀₁
101 ProLeuGluAlaProGlnGlnAlaProGlnProProValAlaProIle₁₁₇
|||
302 CCTTCGATCCCTCAGTGCAACTCAAGCTGCAACACACGATCACTAG₃₅₁
117 ThrSerGlnProGluGlyLeuProAlaGlnAlaProAsnThrHisAsp₁₃₄
|||||
352 CACAGATGCCCA.....ACTACAAATGTGCTGCAGATACCTTATGTC₃₉₅
134 snAlaLysSerAsnLeuSerGlyArgAsnValAspThrIleLea₁₅₀
|||||
396 TGGCTGCTCGAATTTAGTTGCTGGTAGTAATCTTGACGACGACTATTCA₄₄₅
151 GlnLeuMetGluMetGlyGlySerTrpAspLysAspLysValGln₁₆₇
|||||
446 CAATTTATGGACATGGTGCTGGCAATTTGGACAGACACAGTTAGTGG₄₉₅
167 gAlaLeuArgAlaAlaTrpAsnAsnProGluArgAlaValGluTrpLeu₁₈₄
|||||
496 TCGCTTCACAGCAGCTTAAATTAACCCACAGCGCTGATAGATTACTTGT₅₄₅
184 TrpSerGlyLeuProValThrAlaGlnIleAlaValProIle₁₉₇
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546 ATTCTGGAATCCCTGAAAGCAGCAAGATTGCTGCCAGTT₅₈₆
seq_name: gb_est2:BM113219
seq_documentation_block:
LOCUS BM113219 691 bp mRNA linear EST 26-NOV-2001
DEFINITION EST560755 potato roots Solanum tuberosum cDNA clone cPRO17N13 5'
end, mRNA sequence.
ACCESSION BM113219 GI:17076267
VERSION
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; eunasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 691)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Uiterback,T., Chienlung,A., Bougri,O., Buell,C.R., Renning,C.,
Tankley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel.: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: 73.
FEATURES
source
Location/Qualifiers
1..691
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/cultivar="Kennebec"
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/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
BASE COUNT 182 a 158 c 163 g 188 t
ORIGIN
alignment_scores:
Quality: 593.50 Length: 200
Ratio: 3.619 Gaps: 4
Percent Similarity: 82.000 Percent Identity: 61.500
alignment_block:
US-09-805-550-4 x BM113219 ..
Align seg 1/1 to: BM113219 from: 1 to: 691
171 AlaAlaTrpAsnAsnProGluArgAlaValGluTrpLeuTrpSerGly₁₁₇
|||||
1 GCTGATATTAACATCCAGAAAGAGCTATGATTAATCTGATCTGGTAT₅₀
187 eProValThrAlaGluIle.....AlaValProIleGlyGlyGlnGly₂₀₂
|||||
51 TCGTGAGCAAGCAAGAAATCCACACTGCTGCTCGCAGCGGACAGCTG₁₀₀
202 LAsnThrThrAspArgAlaProThrGlyGluAlaGlyLeuSerGly₂₁₈
::|||
101 TAAATCTCCAGTTTCAGGCT..TCACAGCCACAGTTCGCTCCGGTGG₁₄₇
219 ProAsnThrAlaProLeuAspLeuPheProGlnGlyAlaSerAsnAla₂₃₅
|||||
148 CCAAATGCTAATCTTGGATCTTCTCCAGAGGCTTCACAAATGGG₁₉₇
235 YGlyGlyAlaGlyGlyGlyProLeuAspPheLeuAsnAsnProGln₂₅₂
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198 TTCAAATGTTGGAGCTGGAATTTGGATTCTTAACCAATAGTCCACAG₂₄₇
252 heGlnAlaValArgGluMetValHisThrAsnProGlnIleLeuGln₂₆₈
|||||
248 TTCACGCCCTCCGACGAAATGCTCAACCAACCCACAGATATTGCGACCA₂₉₇
269 MetLeuValGluLeuSerLysGlnAsnProGlnIleLeuArgLeuIle₂₈₅
|||||
298 ATGCTCCAGAGTTGGGTAAAGCAAAATCCATATGATGGGCTGATCA₃₄₇
285 uGlnAsnHisAspGluPheLeuGlnIleLeuAsnGluTrpProheGlu₃₀₂
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348 AGAGCATCAAGCTGACTTCTGGCCCTCATCAATGAACCGTTGAG...G₃₉₄
302 YGluGlyAspPheLeuAspGlnProGluGluAspGluMetProHisAla₃₁₈
|||||
395 GGGAAAGGAACGCTCCCTGGGCGACCG...GCAAGGCGCTATACCAACGCT₄₄₁
319 LLeSerValThrProGluGlnGlnAlaIleGlyArgLeuGluSer₃₃₅
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442 GTGACTGTCACACCTGAAGAGCGTGAAGCTATGAACAGCTTAACCTAT₄₉₁
335 tGlyPheAspArgAlaArgValIleGlnAlaPheLeuAlaCysAspArg₃₅₂
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492 GGGTTTCGATCGAGCTTGGTGGCAAGTATTTTGGATGCAACAAAA₅₄₁
352 snGluGluLeuAlaAlaAsnTrpLeuLeuGlnHisAlaGlyGluGlu₃₆₈
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542 ATGAGAGATGGCTGCAAACTATCTGTAGATCACAATGCATGAGTTGAT₅₉₁

